

PK #10



PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/646,561

DATE: 01/22/2002

TIME: 10:18:17

Input Set : A:\Sequencelisting.txt

Output Set: N:\CRF3\01182002\I646561.raw

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5 <110> APPLICANT: Sim, Gek-Kee
7     Yang, Shumin
9     Sellins, Karen S.
13 <120> TITLE OF INVENTION: NOVEL FORMS OF T CELL COSTIMULATORY PROTEINS, NUCLEIC
15     ACID MOLECULES, AND USES THEREOF
19 <130> FILE REFERENCE: IM-1-C1-PCT
C--> 23 <140> CURRENT APPLICATION NUMBER: US/09/646,561
C--> 25 <141> CURRENT FILING DATE: 2000-09-19
29 <150> PRIOR APPLICATION NUMBER: 60/078,765
31 <151> PRIOR FILING DATE: 1998-03-19
35 <150> PRIOR APPLICATION NUMBER: 09/062,597
37 <151> PRIOR FILING DATE: 1998-04-17
41 <160> NUMBER OF SEQ ID NOS: 65
45 <170> SOFTWARE: PatentIn Ver. 2.0
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51 <211> LENGTH: 2830
53 <212> TYPE: DNA
55 <213> ORGANISM: Canis familiaris
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77 gaacatcagc tagatcttcc agcagtaaaa aggaagttgg aaaggggatt gcctctggta 180
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85 tctcagaact ggggcctcat cctttgacgt tttgttttgt tttgttctaa cacaagaaaa 300
89 aaaaaaaaga ggagttatcc ttcagcagca gaagcc atg gat tac aca gcg aag 354
91                                     Met Asp Tyr Thr Ala Lys
93                                     1           5
97 tgg aga aca cca cca ctc aaa cac cca tat ctc aag gtc tct cag ctc 402
99 Trp Arg Thr Pro Pro Leu Lys His Pro Tyr Leu Lys Val Ser Gln Leu
101          10           15           20
105 ttg gtg cta gct agt ctc ttt tac ttc tgt tca ggc atc atc cag gtg 450
107 Leu Val Leu Ala Ser Leu Phe Tyr Phe Cys Ser Gly Ile Ile Gln Val
109          25           30           35
113 aac aag aca gtg aaa gaa gta gca gta ctg tcc tgt gat tac aac att 498
115 Asn Lys Thr Val Lys Glu Val Ala Val Leu Ser Cys Asp Tyr Asn Ile
117          40           45           50
121 tcc act aca gaa ctg atg aaa gtt cga atc tat tgg caa aag gat gat 546
123 Ser Thr Thr Glu Leu Met Lys Val Arg Ile Tyr Trp Gln Lys Asp Asp
125 55          60           65           70
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139 Tyr Glu Asn Arg Thr Phe Ala Asp Phe Thr Asn Asn Leu Ser Ile Val
141          90          95          100
145 att atg gct ctg cgc ctg tca gac aat ggc aaa tac acc tgt atc gtt 690
147 Ile Met Ala Leu Arg Leu Ser Asp Asn Gly Lys Tyr Thr Cys Ile Val
149          105          110          115
153 caa aag act gaa aaa agg tct tac aaa gtg aaa cac atg act tcg gtg 738
155 Gln Lys Thr Glu Lys Arg Ser Tyr Lys Val Lys His Met Thr Ser Val
157          120          125          130
161 atg tta ttg gtc aga gct gac ttc cct gtc cct agt ata act gac ctt 786
163 Met Leu Leu Val Arg Ala Asp Phe Pro Val Pro Ser Ile Thr Asp Leu
165 135          140          145          150
169 gga aat cca tcc cat gac atc aaa agg ata atg tgt tca acc tct gga 834
171 Gly Asn Pro Ser His Asp Ile Lys Arg Ile Met Cys Ser Thr Ser Gly
173          155          160          165
177 ggt ttt cca aag cct cac ctc tcc tgg tgg gaa aat gaa gaa gaa ttg 882
179 Gly Phe Pro Lys Pro His Leu Ser Trp Trp Glu Asn Glu Glu Glu Leu
181          170          175          180
185 aat gct gcc aac aca aca gtt tcc caa gac ccg gac act gag ttg tac 930
187 Asn Ala Ala Asn Thr Thr Val Ser Gln Asp Pro Asp Thr Glu Leu Tyr
189          185          190          195
193 act att agt agt gaa ctg gat ttc aat ata aca agc aac cat agc ttt 978
195 Thr Ile Ser Ser Glu Leu Asp Phe Asn Ile Thr Ser Asn His Ser Phe
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201 gtg tgt ctt gtc aag tat gga gac tta aca gta tca cag atc ttc aac 1026
203 Val Cys Leu Val Lys Tyr Gly Asp Leu Thr Val Ser Gln Ile Phe Asn
205 215          220          225          230
209 tgg caa aaa tca gtc gag cca cac cct ccc aat aac cag caa cag ctc 1074
211 Trp Gln Lys Ser Val Glu Pro His Pro Pro Asn Asn Gln Gln Gln Leu
213          235          240          245
217 tgg gtc atc ctg atc tta gta gta agt ggt gtg att gct gtg atc act 1122
219 Trp Val Ile Leu Ile Leu Val Val Ser Gly Val Ile Ala Val Ile Thr
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245 295          300
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261 gttcaggcct gggaagagac attcggaaaa tacttgtctc attaatagaca aggacatcaa 1508
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277 catctgatgc aacactagaa ggttttgtgt tgctgtcaaa agcaatctga tgctaattgtg 1748
281 tggtagtatg atggtatata taccaatatg agaatgatgg aaaaattact ggggtttact 1808
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289 ggagaaaagta gatctatcca aaactaatat ctgctgacat gtaagatgaa tgacttatat 1928
293 acctcaaagc gatagtcacg ttggagaggg ataggttggg ttagagagtc acatcctact 1988
297 ggttcatatt ggactgataa tctccttaat ggctttatgc tagtttaaac tcatttataa 2048
301 aacatgagaa agttctcatt taaaatgaga taggttttaa ttgtatatta ctaaacagat 2108
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363 <212> TYPE: PRT

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369 <400> SEQUENCE: 2

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379 20 25 30
383 Ser Gly Ile Ile Gln Val Asn Lys Thr Val Lys Glu Val Ala Val Leu
385 35 40 45
389 Ser Cys Asp Tyr Asn Ile Ser Thr Thr Glu Leu Met Lys Val Arg Ile
391 50 55 60
395 Tyr Trp Gln Lys Asp Asp Glu Val Val Leu Ala Val Thr Ser Gly Gln
397 65 70 75 80
401 Thr Lys Val Trp Ser Lys Tyr Glu Asn Arg Thr Phe Ala Asp Phe Thr
403 85 90 95
407 Asn Asn Leu Ser Ile Val Ile Met Ala Leu Arg Leu Ser Asp Asn Gly
409 100 105 110
413 Lys Tyr Thr Cys Ile Val Gln Lys Thr Glu Lys Arg Ser Tyr Lys Val
415 115 120 125
419 Lys His Met Thr Ser Val Met Leu Leu Val Arg Ala Asp Phe Pro Val
421 130 135 140
425 Pro Ser Ile Thr Asp Leu Gly Asn Pro Ser His Asp Ile Lys Arg Ile
427 145 150 155 160
431 Met Cys Ser Thr Ser Gly Gly Phe Pro Lys Pro His Leu Ser Trp Trp
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449 Thr Ser Asn His Ser Phe Val Cys Leu Val Lys Tyr Gly Asp Leu Thr
451          210          215          220
455 Val Ser Gln Ile Phe Asn Trp Gln Lys Ser Val Glu Pro His Pro Pro
457 225          230          235          240
461 Asn Asn Gln Gln Gln Leu Trp Val Ile Leu Ile Leu Val Val Ser Gly
463          245          250          255
467 Val Ile Ala Val Ile Thr Ala Ile Thr Gly Gly Cys Leu Ala His Arg
469          260          265          270
473 Ser Ala Ala Arg Trp Arg Gln Arg Asn Arg Asn Lys Glu Asp Met Asp
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571 cacacattag catcagattg cttttgacag caacacaaaa ccttctagtg ttgcatcaga 1140
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619 gccagttgaa gatctgtgat actgttaagt ctccatactt gacaagacac acaaagctat 1860
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749 ggagacttaa cagtatcaca gatcttcaac tggcaaaaat cagtcgagcc acacctctcc 720
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757 atcactgcca ttacaggagg ctgcctagcc cacagatctg ctgcaagatg gagacagaga 840
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VERIFICATION SUMMARY

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L:23 M:270 C: Current Application Number differs, Replaced Current Application Number

L:25 M:271 C: Current Filing Date differs, Replaced Current Filing Date